

10/547532

SEQUENCE LISTING

sequence_listing.txt

<110> SHINTANI, ET AL.

<120> MEDICINAL USE OF MIP-3 α INHIBITOR AND METHOD OF SCREENING BRAIN/NERVE CELL PROTECTIVE AGENT

<130> 20039.1USWO

<140> New filing

<141> August 31, 2005

<150> PCT/JP2004/002774

<151> 2004-03-04

<150> JP 2003-056885

<151> 2003-03-04

<150> JP 2003-106247

<151> 2003-04-10

<160> 21

<170> PatentIn version 3.1

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Thr Lys Ser Leu Leu Ala Ala Leu Met Ser Val Leu -25-20 -15 cta ctc cac ctc tgc ggc gaa tca gaa
gca gca agc aac ttt gac tgc 96Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala SerAsn Phe Asp Cys -10 -5 -1 1 5
tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc

144Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly

10 15 20 ttc aca cgg cag ctg

gcc aat gaa ggc tgt gac atc aat gct atc atc 192Phe Thr Arg Gln Leu Ala Asn Glu
Gly Cys Asp Ile Asn Ala Ile Ile 25 30

35 ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa

cag act 240Phe His Thr Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr

40 45 50 tgg gtg aaa

tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg 288Trp Val Lys Tyr Ile Val

Arg Leu Leu Ser Lys Lys Val Lys Asn Met 55 60

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sequence_listing.txt

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-10 -5 -1 1 5
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
10 15 20
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
25 30 35
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
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Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
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-15 -10
gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc 96Ala Tyr Leu
Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys -5
-1 1 5 ctc acg tac aca aag aac gtg tat cat
cat gcg aga aat ttt gtg ggt 144Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg
Asn Phe Val Gly 10 15 20
ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct atc atc
192Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile 25
30 35 ttt cac ctg aag tcg
aaa aga tcc gtg tgc gct gac cca aag cag atc 240Phe His Leu Lys Ser Lys Arg Ser
Val Cys Ala Asp Pro Lys Gln Ile 40 45 50
55 tgg gtg aaa agg att ttg cac ctc ctc agc cta aga acc aag
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sequence_listing.txt

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Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly
10          15           20
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
25          30           35
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile
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Gly Gly Lys Arg Leu Leu Phe Leu Ala Leu Ala Trp Val           -25
-20          -15           ctg ctg gct cac ctc tgc agc caq gca
gaa gca gca agc aac tac gac      96Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala
Ser Asn Tyr Asp           -10          -5           -1   1
5          tgt tgc ctc tcg tac ata cag acg cct ctt cct tcc aga gct att gtg
144Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile val
10          15           20           ggt ttc aca aga cag
atg gcc gat gaa gct tgt gac att aat gct atc      192Gly Phe Thr Arg Gln Met Ala Asp
Glu Ala Cys Asp Ile Asn Ala Ile           25           30
35          atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca
aag cag      240Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
40          45           50           aac tgg
gtg aaa agg gct gtg aac ctc ctc agc cta aga gtc aag aag      288Asn Trp Val Lys Arg
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291Met
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Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp

sequence_listing.txt

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Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile			
25 30 35			
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln			
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10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225			
gat tat ttt gtg tca gtc aat act act tca			
tat tac tca gtt gat tct gag 96Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser			
Val Asp Ser Glu 20 25 30			
atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta ttt			
144Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe			
35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225			
gta ccg att gcc tac			
tcc ttg atc tgt gtc ttt ggc ctc ctg ggg aat 192Val Pro Ile Ala Tyr Ser Leu Ile			
Cys Val Phe Gly Leu Leu Gly Asn 50 55			
att ctg gtg gtc atc acc ttt gct ttt tat aag aag gcc agg			
tct atg 240Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met			
65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225			
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gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt 288Thr Asp Val Tyr Leu			
Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val 85			
90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225			
ctt act ctc cca ttc tgg gca gtg agt cat gcc			
act ggt gcg tgg gtt 336Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala			
Trp Val 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225			
ttt aac tgc ggg atg ctg ctc ctg			
act tgc att agc atg gac cgg tac 432Phe Asn Cys Gly Met Leu Leu Thr Cys Ile			
Ser Met Asp Arg Tyr 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225			
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atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc 528Leu Pro Arg Ser Lys Ile Ile Cys			
Leu Val Val Trp Gly Leu Ser Val 170			
175 180 185 190 195 200 205 210 215 220 225			
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acc caa 576Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln			
180 185 190 195 200 205 210 215 220 225			
gac gtc tgt gaa ccc aag tac cag act gtc tcg gag ccc atc 624Gly Ser Asp Val Cys			
Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile 200			
205 210 215 220 225			
agg tgg aag ctg ctg atg ttg ggg ctt gag cta			
ctc ttt ggt ttc ttt 672Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly			
Phe Phe 210 215 220 225			
atc cct ttg atg ttc atg ata ttt tgt tac acg ttc att gtc aaa acc 720Ile Pro			
Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr 225			
230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400			
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agg cac aaa gcc atc cgt gta atc 768Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys			

sequence_listing.txt

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816Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met		
260 265 270 gtc ctg ctt gtg acg		
gct gca aat ttg ggt aaa atg aac cga tcc tgc	864Val	Leu Leu Val Thr Ala Ala Asn
Leu Gly Lys Met Asn Arg Ser Cys	275	280
285 cag agc gaa aag cta att ggc tat acg aaa act gtc aca gaa		
gtc ctg 912Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu		
290 295 300 gct ttc		
ctg cac tgc tgc ctg aac cct gtg ctc tac gct ttt att ggg	960Ala	Phe Leu His Cys
Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly	305	310
315 320 cag aag ttc aga aac tac ttt ctg aag atc ttg		
aag gac ctg tgg tgt	1008Gln	Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu
Trp Cys	325	330
gtg aga agg aag tac aag tcc tca ggc ttc tcc tgt gcc ggg agg tac	1056Val	Arg
Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr		340
345 350 tca gaa aac att tct cgg cag acc		
agt gag acc gca gat aac gac aat	1104Ser	Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr
Ala Asp Asn Asp Asn	355	360
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1122Ala Ser Ser Phe Thr Met		370

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35 40 45		
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn		
50 55 60		
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Ala Arg Ser Met		
65 70 75 80		
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val		
85 90 95		
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val		
100 105 110		
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn		
115 120 125		
Phe Asn Cys Gly Met Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr		
130 135 140		
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr		
145 150 155 160		
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val		
165 170 175		
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln		
180 185 190		
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile		
195 200 205		
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe		
210 215 220		
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr		
225 230 235 240		
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile		
245 250 255		
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met		
260 265 270		

sequence_listing.txt

Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
 275 280 285
 Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
 290 295 300
 Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
 305 310 315 320
 Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
 325 330 335
 Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
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 Ser Leu Glu Glu 20 25 30
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 35 40 45 tgt gtc ttt ggc ctc
 ctg ggc aac att atg gtg gtg atg acc ttt gcc 192Cys Val Phe Gly Leu Leu Gly Asn
 Ile Met Val Val Met Thr Phe Ala 50 55
 60 ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg ttg
 aac atg 240Phe Tyr Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
 65 70 75 80 gcc atc
 aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt 288Ala Ile Thr Asp Ile
 Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val 85
 90 95 act cat gcc acc aac act tgg gtt ttc agc gat
 gca ctg tgt aaa ctg 336Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys
 Lys Leu 100 105 110
 atg aaa ggc aca tat gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg 384Met Lys
 Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu 115
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 Val Gln Ala Thr Lys 130 135 140
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 480Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys 145
 150 155 160 gtg gca gtg tgg ttc
 atc tcc atc atc atc tca agc cct aca ttt atc 528Val Ala Val Trp Phe Ile Ser Ile
 Ile Ile Ser Ser Pro Thr Phe Ile 165 170
 175 ttc aac aag aaa tac gag ctg cag gat cgt gat gtc tgt gag
 cca cgg 576Phe Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu Pro Arg
 180 185 190 tac agg
 tct gtc tca gag ccc atc acg tgg aag ctg ctg ggt atg gga 624Tyr Arg Ser Val Ser
 Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly 195 200
 205 ctg gag ctg ttc ttt ggg ttc ttc acc cct ttg
 ctg ttt atg gtg ttc 672Leu Glu Leu Phe Phe Gly Phe Phe Thr Pro Leu Leu Phe Met
 Val Phe 210 215 220
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sequence_listing.txt

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 atc gct gtg gtt ctc gtg ttc ctg 768Arg His Arg Ala Ile Arg Val Val Ile Ala Val
 Val Leu Val Phe Leu 245 250
 255 gct tgt cag atc cct cac aac atg gtc ctc ctc gtg act gcg gtc aac
 816Ala Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Val Asn
 260 265 270 acg ggc aaa gtg ggc
 cggtc acc acc gag aaa gtc ctc gcc tac 864Thr Gly Lys Val Gly Arg Ser Cys
 Ser Thr Glu Lys Val Leu Ala Tyr 275 280
 285 acc agg aac gtg gcc gag gtc ctg gct ttc ctg cat tgc tgc
 ctc aac 912Thr Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn
 290 295 300 ccc gtg
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 Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Met 305 310
 315 320 aag atc atg aag gat gtg tgg tgt atg aga agg
 aag aat aag atg cct 1008Lys Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys
 Met Pro 325 330 335
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 35 40 45
 Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
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 Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
 65 70 75 80
 Ala Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
 85 90 95
 Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys Lys Leu
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 Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu
 115 120 125
 Ala Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys
 130 135 140
 Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys
 145 150 155 160
 Val Ala Val Trp Phe Ile Ser Ile Ile Ser Ser Pro Thr Phe Ile
 165 170 175
 Phe Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu Pro Arg
 180 185 190
 Tyr Arg Ser Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly
 195 200 205
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 210 215 220
 Cys Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys
 225 230 235 240
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 245 250 255
 Ala Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Val Asn

sequence_listing.txt

260	265	270	
Thr Gly Lys Val Gly Arg Ser Cys	Ser Thr Glu Lys Val Leu Ala Tyr		
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Thr Arg Asn Val Ala Glu Val	Leu Ala Phe Leu His Cys Cys Leu Asn		
290	295	300	
Pro Val Leu Tyr Ala Phe Ile Gly Gln Lys	Phe Arg Asn Tyr Phe Met		
305	310	315	320
Lys Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys Met Pro			
325	330	335	
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<223> Oligonucleotide designed to act as primer for amplifying fragment of rat MIP-3 β gene transcript.

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<210> 12
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<210> 13
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<222> (343)..(1443)
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aagcactaag gcgggggtac 300ctggccagcc cacttcggag ctcagcgttt ccttggaaa cg atg aat
ttc acc 354 Met Asn Phe Thr
1 gag gcc
aac tac gga atg gaa gat tat act ggc tca gat tac tct atg 402Glu Ala Asn Tyr Gly
Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met 5 10
15 20 ttt cca gag acc gag cca tgc tct ctg caa gag
gtc aga gac ttc acc 450Phe Pro Glu Thr Glu Pro Cys Ser Leu Gln Glu Val Arg Asp
Phe Thr 25 30 35

sequence_listing.txt

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45				50										ctt	ggc	aat	att	atg	gtg	gtg	ata											
acc	ttt	gcc	ttc	tac	aag	aaa	gcc							546	Leu	Gly	Asn	Ile	Met	Val	Val	Ile	Thr	Phe	Ala							
Phe	Tyr	Lys	Lys	Ala				55						60							65											
agg	tcc	atg	act	gac	gtc	tac	cta	ttg	aac	atg	gcc	atc	aca	gac	ata																	
594	Arg	Ser	Met	Thr	Asp	Val	Tyr	Leu	Leu	Asn	Met	Ala	Ile	Thr	Asp	Ile		70														
75				80											ctc	ttt	gtc	ctc	acc													
cta	cca	ttc	tgg	gca	gtt	act	cat	gcc	act	gac				642	Leu	Phe	Val	Leu	Thr	Leu	Pro	Phe										
Trp	Ala	Val	Thr	His	Ala	Thr	Asp		85					90							95											
100															act	tgg	atc	ttt	ggc	aac	acg	atg	tgt	aaa	ctg	atg	aaa	ggc				
acg	tat		690	Thr	Trp	Ile	Phe	Gly	Asn	Thr	Met	Cys	Lys	Leu	Met	Lys	Gly	Thr	Tyr													
105				110										115							gct	gtc										
aac	ttt	aac	tgt	ggg	atg	ctg	ctc	ctg	gcc	tgt	atc	agc	atg		738	Ala	Val	Asn	Phe	Asn												
Cys	Gly	Met	Leu	Leu	Leu	Ala	Cys	Ile	Ser	Met				120																		
125				130										130	gac	cgg	tac	att	gcc	atc	gtc	cag	gcg	acc	aaa							
tct	ttc	cgg	gta	cgc										786	Asp	Arg	Tyr	Ile	Ala	Ile	Val	Gln	Ala	Thr	Lys	Ser	Phe	Arg				
Val	Arg				135									140								145										
tcc	aga	aca	ctg	acg	cac	agt	aag	gtc	atc	tgt	ctg	acg	gtg	tgg	ttc		834	Ser	Arg													
Thr	Leu	Thr	His	Ser	Lys	Val	Ile	Cys	Leu	Thr	Val	Trp	Phe		150																	
155				160										160	gtt	tcc	atc	atc	atc	tca	agc	ccc										
aca	ttc	tcc	tcc	aac	aag	caa	tac							882	Val	Ser	Ile	Ile	Ile	Ser	Ser	Pro	Thr	Phe	Phe							
Phe	Asn	Lys	Gln	Tyr				165						165						170		175										
180														180	aag	ctg	cag	ggc	cgt	gat	gtc	tgc	gag	cct	cag	tac	aag	ctc	gtc	tcg		
930	Lys	Leu	Gln	Gly	Arg	Asp	Val	Cys	Glu	Pro	Gln	Tyr	Lys	Leu	Val	Ser																
185								190						190						195												
aaa	ctg	ctg	ggc	atg	gga	ctc	gag	ctg	ctc	ttt				978	Glu	Pro	Ile	Thr	Trp	Lys	Leu	Leu										
Gly	Met	Gly	Leu	Glu	Leu	Leu	Phe							200							200		205									
210														210	ggc	tcc	tcc	atc	cct	ttg	ctg	ttt	atg	gtg	ttc	tgt	tac	ctg				
ttc	atc													1026	Gly	Phe	Phe	Ile	Pro	Leu	Leu	Phe	Met	Val	Phe	Cys	Tyr	Leu	Phe	Ile		
215														215						220		225								atc	aag	
acc	ttg	gtg	cag	gcc	cag	aat	tcc	aag	agg	cac	aga	gcc	atc		1074	Ile	Lys	Thr	Leu	Val												
Gln	Ala	Gln	Asn	Ser	Lys	Arg	His	Arg	Ala	Ile				230						230		235										
240														240	cga	gtc	gtg	att	gct	gtg	gtt	ctc	gtg	ttc	ctg							
gct	tgt	cag	atc	cct				1122	Arg	Val	Val	Ile	Ala	Val	Val	Leu	Val	Phe	Leu	Ala	Cys	Gln										
Ile	Pro				245				250					250						255			260									
cac	aac	atg	gtc	ctc	ctc	gtg	act	gca	gcc	aac	acg	ggc	aaa	atg	ggc		1170	His	Asn													
Met	Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Thr	Gly	Lys	Met	Gly		270						275									265		
270														270	cgc	agc	tgc	agc	gcc	gag	aaa	gcc										
ctc	gcc	tac	gcc	agg	aat	gtg	gct							1218	Arg	Ser	Cys	Ser	Ala	Glu	Lys	Ala	Leu	Ala	Tyr							
Ala	Arg	Asn	Val	Ala										280						280		285								290		
gag	gtc	ctg	gct	ttc	ctg	cac	tgc	tgt	ctc	aac	ccc	gtg	ttg	tat	gcc																	
1266	Glu	Val	Leu	Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro	Val	Leu	Tyr	Ala		295		300		305										
ttc	aga	agc	tac	tcc	atg	aag	atc	atg	aag	gat				1314	Phe	Ile	Gly	Gln	Lys	Phe	Arg	Ser										
Tyr	Phe	Met	Lys	Ile	Met	Lys	Asp							310						315												
320														320	gtg	tgg	tgt	atg	agg	agg	aag	agc	aag	gtg	cct	acc	ttc	ttc				
tgt	gcc													1362	Val	Trp	Cys	Met	Arg	Arg	Lys	Ser	Lys	Val	Pro	Thr	Phe	Cys	Ala			
325														325						330		335		340		cggtt						
tac	tca	gaa	agc	tac	tcc	agg	cag	acc	agt	gag	act	gta		1410	Arg	Val	Tyr	Ser	Glu													
Ser	Tyr	Ile	Ser	Arg	Gln	Thr	Ser	Glu	Thr	Val				350						355									345			
350														350	gaa	aat	gac	aac	gca	tcg	tcc	ttt	acc	atg	taa							
cac	gag	agc	caa	agg	cag	act	tcc	agg	cag	acc	agt	gag	act	gta	1463	Glu	Asn	Asp	Asn	Ala	Ser	Ser	Phe	Thr	Met							
														360						365												
tgccccgaaa	gcctttgtga	aacttgctat	tacatgtga																													

1502

<210> 14

<211> 366

<212> PRT

<213> Rattus norvegicus

<400> 14

Met Asn Phe Thr Glu Ala Asn Tyr Gly Met Glu Asp Tyr Thr Gly Ser

sequence_listing.txt

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Asp	Tyr	Ser	Met	Phe	Pro	Glu	Thr	Glu	Pro	Cys	Ser	Leu	Gln	Glu	Val
			20					25				30			
Arg	Asp	Phe	Thr	Lys	Val	Phe	Val	Pro	Ile	Ala	Tyr	Ser	Leu	Ile	Cys
			35				40				45				
Val	Phe	Gly	Leu	Leu	Gly	Asn	Ile	Met	Val	Val	Ile	Thr	Phe	Ala	Phe
			50				55				60				
Tyr	Lys	Lys	Ala	Arg	Ser	Met	Thr	Asp	Val	Tyr	Leu	Leu	Asn	Met	Ala
			65			70				75				80	
Ile	Thr	Asp	Ile	Leu	Phe	Val	Leu	Thr	Leu	Pro	Phe	Trp	Ala	Val	Thr
							85		90				95		
His	Ala	Thr	Asp	Thr	Trp	Ile	Phe	Gly	Asn	Thr	Met	Cys	Lys	Leu	Met
							100		105				110		
Lys	Gly	Thr	Tyr	Ala	Val	Asn	Phe	Asn	Cys	Gly	Met	Leu	Leu	Leu	Ala
			115				120				125				
Cys	Ile	Ser	Met	Asp	Arg	Tyr	Ile	Ala	Ile	Val	Gln	Ala	Thr	Lys	Ser
			130			135				140					
Phe	Arg	Val	Arg	Ser	Arg	Thr	Leu	Thr	His	Ser	Lys	Val	Ile	Cys	Leu
			145			150				155				160	
Thr	Val	Trp	Phe	Val	Ser	Ile	Ile	Ile	Ser	Ser	Pro	Thr	Phe	Phe	
						165			170				175		
Asn	Lys	Gln	Tyr	Lys	Leu	Gln	Gly	Arg	Asp	Val	Cys	Glu	Pro	Gln	Tyr
			180				185					190			
Lys	Leu	Val	Ser	Glu	Pro	Ile	Thr	Trp	Lys	Leu	Leu	Gly	Met	Gly	Leu
			195				200					205			
Glu	Leu	Leu	Phe	Gly	Phe	Phe	Ile	Pro	Leu	Leu	Phe	Met	Val	Phe	Cys
			210			215					220				
Tyr	Leu	Phe	Ile	Ile	Lys	Thr	Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg
			225			230				235				240	
His	Arg	Ala	Ile	Arg	Val	Val	Ile	Ala	Val	Val	Leu	Val	Phe	Leu	Ala
						245			250					255	
Cys	Gln	Ile	Pro	His	Asn	Met	Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Thr
						260			265				270		
Gly	Lys	Met	Gly	Arg	Ser	Cys	Ser	Ala	Glu	Lys	Ala	Leu	Ala	Tyr	Ala
						275			280			285			
Arg	Asn	Val	Ala	Glu	Val	Leu	Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro
			290			295					300				
Val	Leu	Tyr	Ala	Phe	Ile	Gly	Gln	Lys	Phe	Arg	Ser	Tyr	Phe	Met	Lys
			305			310				315				320	
Ile	Met	Lys	Asp	Val	Trp	Cys	Met	Arg	Arg	Lys	Ser	Lys	Val	Pro	Thr
						325			330				335		
Phe	Phe	Cys	Ala	Arg	Val	Tyr	Ser	Glu	Ser	Tyr	Ile	Ser	Arg	Gln	Thr
						340			345				350		
Ser	Glu	Thr	Val	Glu	Asn	Asp	Asn	Ala	Ser	Ser	Phe	Thr	Met		
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<210> 15
<211> 1309
<212> DNA
<213> Ratt

<220>
<221> CDS
<222> (150) .. (1250)
<223>

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 aggactggag cctggacaag cactaaggcg ggggtacctg gccagccccac 120ttcggagctc agcgttcct
 tggaaacg atg aat ttc acc gag gcc aac tac 173
 Met Asp Phe Thr Glu Ala Asn Tyr 1

Met Asn Phe Thr Glu Ala Asn Tyr
 5 gga atg gaa gat tat act ggc tca gat tac tct atg ttt cca
 gag acc 221Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met Phe Pro Glu Thr

sequence_listing.txt

10	15	20	gag cca
tgc tct ctg caa gag gtc aga gac ttc acc aag gtg ttc gtg		269Glu Pro Cys Ser Leu	
Gln Glu Val Arg Asp Phe Thr Lys Val Phe Val	25	30	
35	40	cca atc gcc tac tcc tta atc tgt gtc ttt ggc	
ctc ctt ggc aat att	317Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly		
Asn Ile	45	50	
atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc agg tcc atg act	365Met Val		
Val Ile Thr Phe Ala Phe Tyr Lys Ala Arg Ser Met Thr	60		
65	70	gac gtc tac cta ttg aac atg gcc	
atc aca gac ata ctc ttt gtc ctc	413Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp		
Ile Leu Phe Val Leu	75	80	
acc cta cca ttc tgg gca gtt act cat gcc act gac act tgg atc ttt	85		
461Thr Leu Pro Phe Trp Ala Val Thr His Ala Thr Asp Thr Trp Ile Phe	90		
95	100	ggc aac acg atg tgt	
aaa ctg atg aaa ggc acg tat gcg gtc aac ttt	509Gly Asn Thr Met Cys Lys Leu Met		
Lys Gly Thr Tyr Ala Val Asn Phe	105	110	
120	aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg gac cg		
tac att	557Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met Asp Arg Tyr Ile		
125	130	135	
gtc cag gcg acc aaa tct ttc cgg gta cgc tcc aga aca ctg	605Ala Ile Val Gln Ala		
Thr Lys Ser Phe Arg Val Arg Ser Arg Thr Leu	140		
145	150	acg cac agt aag gtc atc tgt ctg acg gtg tgg	
ttc gtt tcc atc atc	653Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe Val Ser		
Ile Ile	155	160	
165	atc tca agc ccc aca ttc ttc aac aag caa tac aag ctg cag ggc		
Ser Pro Thr Phe Phe Asn Lys Gln Tyr Lys Leu Gln Gly	701Ile Ser		
175	180	cgt gat gtc tgc gag cct cag tac	
aag ctc gtc tcg gag ccc atc acg	749Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val		
Ser Glu Pro Ile Thr	185	190	
195	200	tgg aaa ctg ctc ggc atg gga ctc gag ctg ctc ttt ggc ttc ttc atc	
797Trp Lys Leu Leu Gly Met Gly Leu Glu Leu Leu Phe Gly Phe Phe Ile			
205	210	215	
gtg ttc tgt tac ctg ttc atc atc aag acc ttg	845Pro Leu Leu Phe Met Val Phe Cys		
Tyr Leu Phe Ile Ile Lys Thr Leu	220		
225	230	235	
gtg cag gcc cag aat tcc aag agg cac aga gcc atc cga gtc			
gtg att	893Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile Arg Val Val Ile		
235	240	245	
gtt ctc gtg ttc ctg gct tgt cag atc cct cac aac atg gtc	941Ala Val Val Leu Val		
Phe Leu Ala Cys Gln Ile Pro His Asn Met Val	250		
255	260	ctc ctc gtg act gca gcc aac acg ggc aaa atg	
ggc cgc agc tgc agc	989Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly Arg Ser		
Cys Ser	265	270	
275	280	285	
gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct gag gtc ctg gct	1037Ala Glu		
Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala Glu Val Leu Ala			
290	295	ttc ctg cac tgc tgt ctc aac ccc	
gtg ttg tat gcc ttc att gga cag	1085Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr		
Ala Phe Ile Gly Gln	300	305	
310	aaa ttc aga agc tac ttc atg aag atc atg aag gat gtg tgg tgt atg		
1133Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp Val Trp Cys Met			
315	320	325	
gtg cct acc ttc ttc tgt gcc cgg gtt tac tca	1181Arg Arg Lys Ser Lys Val Pro Thr		
Phe Phe Cys Ala Arg Val Tyr Ser	330		
335	340	gaa agc tac atc tcc agg cag acc agt gag act gta gaa aat	
gac aac	1229Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val Glu Asn Asp Asn		
345	350	355	
tcc ttt acc atg taa cacgagagca caaaggcagca tgccccgaaa	1280Ala Ser Ser Phe Thr		
Met	360	365	
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gcctttgtga aacttgctat tacatgtga			

1309

<210> 16
<211> 25
<212> DNA

sequence_listing.txt

<213> Artificial
<220>
<223> Oligonucleotide designed to act as primer for amplifying CCR6 cDNA derived from rat kidney.

<400> 16
tgtattgaag acagaacact tgtgg 25

<210> 17
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying CCR6 cDNA derived from rat kidney or rat liver.

<400> 17
tcacatgtaa tagcaagttt cacaaagg 28

<210> 18
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying CCR6 cDNA derived from rat liver.

<400> 18
gcatctcaact acccgctctc c 21

<210> 19
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying fragment of rat CCR6 gene transcript.

<400> 19
ggacgatgcg ttgtcatttt c 21

<210> 20
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying fragment of rat CCR6 gene transcript.

<400> 20
ccgcagctgc agcgccgaga aa 22

<210> 21
<211> 20
<212> DNA
<213> Artificial

<220>

sequence_listing.txt
<223> Oligonucleotide designed to act as primer for amplifying fragment of
rat CCR6 gene transcript.

<400> 21
gtgccgggt ttactcagaa 20